

9	809.38	61.79	11.11	97	S71333
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12	782.36	60.1	10.92	9	AF03446
13	782.36	60.1	10.92	9	AF72023
14	769.2	59.0	10.5	9	AF93448
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20	679.2	52.1	14.55	97	HMM372
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22	678.18	52.1	13.83	9	AF048515
23	669.38	51.4	25.3103	6.2	AC012518
24	645.36	49.5	15.00	9	AF075307
25	645.36	49.5	15.00	94	MUSC148
26	645.36	49.5	15.00	94	MUSC148
27	617.8	47.4	10.53	89	AF1970007
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36	498.8	40.6	5.14	88	AF057429
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38	497.2	40.6	5.14	88	AF057434
39	494	40.2	5.14	88	AF057447
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44	477.2	28.8	5.05	88	AF057446
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FYVMALAEGLPTGVNLITGFPRGILDKDKRIDKLDAWDHSHTLNKTLINKPKILL-
PEYEMVGLGLFDLIRKMSWGPIREKVENYNN"
BASE COUNT      493 a    450 c   479 g    406 t
ORIGIN          144 bp upstream of hpi1 site.

Query Match      87.0% Score 1143.6; Dh 7; Length 1828;
Best Local Similarity 95.4%; Pred. No. 1.5e 273;
Matches 1179; Conservative 0; Mismatches 94; Indels 4; Gaps 12

QY      68 gaat caaaacagccgaccttgcgtctcccaaccggactccttcgaagaacgaatc 127
        ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       443 GGATGCACCAAGATTCGAATTGTCTTGGTCCGCAATCTTGGCTGCTTTGGACAAACGACATC 402

QY      128 tcaataaacattgcattttgccttttaacctggaaaggaaagcaaatcaatgaatga 187
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Db       403 TCAGTAGAAGACTGTGTACTCTTTGGCTTTTAATCTAACAAAGCAAGAACATGCAATGAGGAG 462

QY      188 aaataaataaatgtcaaaagaaaatgaattcgtcaatgcagtgttcgaatgatcatt 247
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Db       463 AATAATATCATGCTAAAGCAAAAGATGCTGTAAATGCGATTGTCGCAATTCGCAAT 522

QY      248 atttgtatttgaaataatatccaaagcccgaagaaccttatctcgataaacccaaca 307
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Db       523 GTTGTGTTTTGGAAATATATGCCAACCTCGAAGAGCTTTTGTCTGTGATAAACCCTATA 582

QY      308 aaaaaacccgaagatccagtcgagcagcaacattcgaagaagctgcattgattccgaatga 367
        ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       583 TTTTCCCAAGCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 649

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[illegible]

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Db	760	GTCATCATACACAGTCGAAAGTCTCAGTCGCTCGGAAAGGACCTTACACACAGACGCTCTT	819
QY	548	ttgaagcattactacgcgcgaagcagaagaattacgcctcgcgcgaagcgttttgcgcgttcaga	607
Db	820	TTAGACATATATATATGCGCAAGCAGAAATATACGCTGAGCTGCGCTTCGCGAGTTCGAC	879
QY	608	gaattacattgaagcattacttgaaggaattcttgaagctcgtctgaataagcagctctatgatt	667
Db	880	AGATACATTCGAGCATATCTTGGACGAGGTCCTTAACTCTGCTATATAGACCTTCATGATG	939
QY	668	ggtccacgaagctcctcttaccgtcatggtggaagcagcctccgaagatgaccttgaataag	727
Db	940	GCGCAGCGACGTCATCTTTATATCATGCTAGCATGATCTCTCCAGGACAGGCTTGATACAG	999
QY	728	cttgaagcctcttgaagctccttcaaaatgatttgaagtcgaagcctgaaggaagattgaacagac	787
Db	1000	TTCGGCTGCTGTCGCTGCTCTTCAGAGCTTTAAGATCAAGCTTCGACAAACAGCTGGCAGCA	1059
QY	788	gttcagcatgattgcgaattgaagacccatcgaagagagcattgtgacccagctctcgaagcgtgaag	847
Db	1060	ATTCGATCATGATGCGCATGAAAGCATATCGGAGGAGACACATTCCTGAGCTGCAATTCGATGATGAC	1119
QY	848	gtttgaattctctctctcgaatgaaagtggaagcgaagcctctcaaaagcgaattctcgaattgagag	907

DB 1120 GTTACTTCCTTTTGTGATGATGTGACCAAGTCTTCCAAAGTAAGTTGGGTGAG 1179
 QY 908 arccctggatgagtcgttggcccgagctacagagcctgtgttacaagcaatcccatag 967
 DB 1180 ACCCTGGGCGAGTCGTGGCCGAGCTACAAAGCTGTGTGTACAGGAGATGCCAATGAC 1239
 QY 968 ttacttaagaagaagcaagaatctgcagatataccctctcgaagaagatllt 1027
 DB 1240 TTCACCTACGAGAGGCGGAGAGAGCTGTCCAGCATATTCCTTGGCGCAAGGCAATTT 1299
 QY 1028 taataccagcagccatlltttggggaacacccactcagctccttaacatacccaaga 1087
 DB 1300 TATTACCATGACACCATTTTGGGGGAAACCCACCTCAGCTCCTTAACATCCAGGAA 1359
 QY 1088 tgccttaaaagatctctcaagcaagaataatgacatagaagcccaatggcatatgag 1147
 DB 1360 TGGTTAAAGCAATCTCCAGGACAGAAAGAAATGACATGAACCCCAATGCGATGTGA 1419
 QY 1148 agccactaaacaagatcttctctcaacaacccactaaatcttaccggagatac 1207
 DB 1420 AGCCATCTAACAGATATTTCTCTTCACCAAAACCTACTATAAACTTATCCCGAATAC 1479
 QY 1208 tgcctgagatatacatataagcctacctgcagatataagcttgcagaatctcttgcag 1267
 DB 1480 TGGTGGATATTCACATAGGCTACTCTCGAGATATTAGCTTGTCAAGATGCTTGGCAG 1539
 QY 1268 arcgaagatataatgtgttgaataaataaactctga 1303
 DB 1540 ACMAAGAGATATAATGTGTAAATAATATGTGTA 1575

RESULT 2

LOCUS AR066334 1828 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 8 from patent US 5849991.
 ACCESSION AR066334
 VERSION AR066334.1 GI:5996550
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1828)
 AUTHORS d'Almeida, J.F., Fearse, M.J., Robins, A.J., Crawford, R.J. and
 Ratliff, P.D.

TITLE Mice homozygous for an inactivated alpha 1,3-galactosyl
 transferase gene

JOURNAL Patent: US 5849991-A 8 15-DEC-1998;
 FEATURES Location/Qualifiers

source 1..1828 /organism "unknown"

BASE COUNT 493 a 450 c 479 g 406 t
 ORIGIN

Query Match 87.0%; Score 1133.6; DB 9; Length 1828;
 Best Local Similarity 95.4%; Pred. No. 1.5e-273;

Matches 117; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

QY 68 ggaatcagaagctgtacactgtctctcccaagccctcctcctctcgaagaagagc 127
 DB 343 GAGGTGAGAGGCTGCACCTCTGCTCTCCAGCCCTGCTCTCTCTGAGAGAGGAG 402
 QY 128 tcaatgaacttgaacttcttgccttctactctggaagagagagagagagagag 187
 DB 403 TCAGTAGAAGCTGTGACTTGTCTTTACTCTAGAGAGAGAGAGAGAGAGAGAG 462
 QY 188 aaaaataaataaataaataaataaataaataaataaataaataaataaataaataa 247
 DB 463 AAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522
 QY 248 gtgtgttttggagatataatcccaagccagaagagctcttctcgaataaaccatca 307
 DB 523 GTTGTGTTTGGAGATATATCCAGAGCCAGAGAGGCTCTTGTGTGATAAAGCCATCA 582

QY 308 aaaaacccagaagctcagtggaagagagagatcgaagaagagctatgtttccgaatga 367
 DB 583 AGAAACCCAGAGAGT---TGTGGCAGAGACATTCAGAAAGGCTGTGTCTTCCAGATAG 639
 QY 368 ttactaatgtgttaccagaagaagaatgaagcgttaagcagaagaagaagaagaaga 427
 DB 640 TTTACCAATGTTACCATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 699
 QY 428 gaagcaaaagcaagcttaagctatcgactgtatcaacccatitaaagccctgaagt 487
 DB 700 GAAGAGCAAGAGCAAGCTTAAAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
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 DB 760 GTACCATGAG 819
 QY 548 ttagagatctactacgaagaagaatctacgtcagccctgaagcttttgcgtcaga 607
 DB 820 TTAGCAATATTATGCGAG 879
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 DB 880 AGATACATGAG 939
 QY 668 ggcacccagatcacttcttactgaagctgtgaagcgtctcgaagaagcttgaaga 727
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 DB 1000 TTGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059
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 DB 1420 AGCCATCTAACAGATATTTCTCTTCACCAAAACCTACTATAAACTTATCCCGAATAC 1479
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 QY 1268 arcgaagatataatgtgttgaataaataaactctga 1303
 DB 1540 ACMAAGAGATATAATGTGTAAATAATATGTGTA 1575

RESULT 3

AF221508 3684 bp mRNA MAM 04-FEB-2001
 LOCUS

QY	240	ctgcatatgttgatctttagaaatatactccagcccccagaagagctctcttctctgaaata	29
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QY	300	accctcatgaataaccagaagatctgctgacgcacgcacatctcgaagtgatctgttgcttc	359
DB	122	ACCGAGTCAAAAAACCCCAAAAT-----TCCCAACACTGCTCAAGAGGAGTGGTGGTTTC	175
QY	460	cgatattgatttaagaatq-----qttaccagaagaagaatgaaatcgttaagaag	410
DB	176	CGAGTACTTAAATAATGCGACTTCACAGTTACCAAGCAAGAAAGAAAGCAAGCAATAGGCAAC	235
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QY	468	catttaagcgcctcgtgaagcttctgctatgaacagatltgaagagcaccctgtgtgtgaag	527
DB	295	CTGAGAAACCGCCGAGAGTGGTGGTCCATACCGAGATACGAGAGCCCTCCAGTGGATGGGAAG	355
QY	528	gcatttcaagaagaagcgcctcttaagcatttaacgcacgcagaagagaataatccgctgcgc	587
DB	356	GCACCTTACACACGACGCGCTCTTAATTAATTATATGCAACACGAATAATATCCGTGGGCT	415
QY	588	tgaacgtttttgcgcgttcgaagaatatacttaagatlaacttgaagagatcttctaaagctga	647
DB	416	TGACGGTCTTTGCTCTGTGGAAAGATACATTCAGCATTACTTGGAGAGGTTCTTAAATATCTG	475
QY	648	ctaataaacatctcgtgaagcttggtgcgcgcgaagctcatcttcaatcattgattgaagacgtct	707
DB	476	CAAAATACATATCTTATGCTTGGTGCACAAAGTCATCTTTACATCATCTGGTATGATATATCT	535
QY	708	cgaagatgcctttatagaagctttagcgccctcgcgcctctcgaagatgatttgaagtcgaag	767
DB	536	CGACGATTCGCTTTCAACAGAGTGGGTCCTCTGCTCATGACAGTGGATACAGTCTTCC	595
QY	768	ctgaagaagaatltgaagaagaatcagatgagatgagatgaagaacacatctgaagaagacatag	827
DB	596	CGGAAACAGCTGGCAAGATATACGATATGAGTATGAGCATGAAGACCATTCGGGACACATCTCC	655
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DB	656	TGGCCCATATCCACACCGAGGTGGACTTTCCTCTCTCATGACAGTGGATACAGTCTTCC	715
QY	888	aagagcgaatltcgtgattcgaagaccccttggttgatctgcgtgcgcacgcatacagccctgtggt	947
DB	716	AAAACAACTTGTGGGAGTGGAGCCCTGGGCCAGTGGTGGCTACACTACAGGCCCTGGTGGT	775
QY	948	acgaagcgaatctcccgatggaatttaacttaaggaagagcgcaaggaagctctgcacatacaatc	1000
DB	776	ACAAAGCCCATCTCTACCCAGTTCACCTTACAGAGAGGCGGAAAGATCCGCACTTACATTC	835
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DB	836	CGTTGGGCTAGGGGATTTTATTAACACAGAGGCCATTTTTGGGGGCAACACCACTATAGC	895
QY	1068	lecttaacatcaccctgaagaatggtctcaagaagaatctcgaagacagaagaatgacataag	1122
DB	896	TTCTAAATATACCTTAGAGAGTCTTTCAAGGCAATCTCTCCAGGCAAGAAAGATAGACATAG	955
QY	1128	aagcccaatgacatcgaatgaagatccatctaaagaagatcttcctctgaagaagaccgaata	1188
DB	956	AAAGCCAGTGGCATATGATGAAGAAGCATCTTAACCAAGTATTTCTCTTCTCAACAAACCCACTA	1010
QY	1188	aaatcttctcccggaatcgtcgtgcgattatatactatataagagcttaacctggaatattaagc	1244
DB	1016	AAATCTTATCCGCAAAATATCTGTGGCATTAATATATAGCATGTCTGTGGATATATAGGA	1078
QY	1248	ttgtcgaagatgctcttgaagaacaaagaatataatcgtgcttagagaataaacgctctga	1303
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RESULT      7
A69344
LOCUS      A69344      1128 bp      DNA
DEFINITION Sequence 1 from patent WO9802453.
ACCESSION  A69344
VERSION    A69344.1  GI:4760171
KEYWORDS
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 1128)
AUTHORS   Gould, P., Robberecht, P., Vandemeers, A. and Woelbroek, M.
TITLE      PEPTIDIC LIGANDS HAVING A HIGHER SELECTIVITY FOR THE VIP1 RECEPTOR
           THAN FOR THE VIP2 RECEPTOR
JOURNAL    PATENT: WO 9802453-A 1 22-JAN-1998;
           UNIV BRUXELLES (BE)
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BASE COUNT      335 a      236 c      266 g      271 t
ORIGIN

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Query Match	65.7%	Score 856.6	DB %	Length 1128
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QY	187	gaaaataatgaatgatacaaggaadaadtaattctgtcgaatgctgattatcttcaactgcat	240	
DB	6	GAAAATATGATGATCCAAAGSAGACAGTGTCTGTGCAATGCTGCTTGCTGCTCAATGTAAI	65	
QY	247	tcctgtgtcttcgggaatataatccagcccggaagcgtcttttgccttgaataacccacac	306	
DB	66	GCCTGTGCTTTCGCAATACATCAACAGCCCGCAAGGTCCTTTGTTTCGATATACCGATC	125	
QY	307	aagaaaccccaaaatcgaatgcgcgcgaacgaatctcgaagaqgcgtgaatcttcgaagat	466	
DB	126	AAAAAACCCACAGACT-----TGGCAGTAGTCCTCAAGGGCCCTGTGCTTCGCACTG	179	
QY	367	gttatacaatg-----gtaccgaagaagaatgaagaagcctgaagcaaaabaaga	417	
DB	180	GTTTACATATGGATCTGCATCACTTACCCAGCAAGCAAGCAAGCTTATAGCGACCAAAAGCA	233	
QY	418	acaaagaagaagaagcaaa--aaagcaagcttaagctatcgactgaatcgaacccattaa	474	
DB	240	ACAAAGAAACAGACACACAGACAGAGAGACTTCCTCACTAGTCGCTGTTATCTCTGAAA	299	
QY	475	acgcctctgaatctgaactatgaatgaatgaagaacccgaatgaatgaagaagactta	534	
DB	300	ACGCCACAGAGCTCGTGACCATTAACCAATGATGAGAGCTCCATCTGGTATACGCAAGGCACTTA	459	
QY	535	caacagagcgcctctagaagcgttactacgcgcgaagcgaagaatctaacctgcgcctgaat	594	
DB	360	CAACGAGACCGCTTGATTAATTATTATGCCCAACACAAAAATTACGCTGGGCTTGACGGT	419	
QY	595	ttctgccttcggaatatacatatgaatctacttgaagaattcttaagctctgaatataa	654	
DB	420	TCTTCTCTCTCGAAGCATATCATTTGACCATTACTTGGAGAGAGCTTTTAATATCTGTAAATAC	479	
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[illegible]

Query Match	65.7%	Score 856.6	Dh 9	Length 1128
Host Local Similarity	87.0%	Prot. No. 4	Loc 2004	
Matches	982	Conserved locs	0	Mismatch 129
			Indels	18
			Gaps	4
Query 187	gaagatattgaatgatacgaaggaagatgattctctcattgctggttatctcgaatgcat	246		
Dh 6	caaaatattgaatgctgcaaaagcaaaatgctgttgcgaatgctgcttgcttgcaatgctgaa	65		
Query 247	tatttatttcttgaagattctatctcgaagccgaagatctttttttctgaatgaacacac	306		
Dh 66	gattctgttttgcgtatgacatgacacaccccaaaatgcttcttgctgtgcgaatgacacgc	125		
Query 407	aaagaaacacgaatcgaatgacgagcagcagcagcagcagcagcagcagcagcagcagc	366		
Dh 126	aaaaaacctacgaatgcttgcgaagacacgctgcgaagcagcagcagcagcagcagcagc	179		
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Dh 180	gttttgaagctg-----gttttgaagctggttgcgaatgacacgaagcagcagcagc	239		
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Dh 240	acgaaggaaggaagaaac	299		
Query 475	acgcctcgaagcttatgactatgacgaattggaagacacacacacacacacacacacac	534		
Dh 300	acgcctcgaagcttatgactatgacgaattggaagacacacacacacacacacacacac	359		
Query 535	caaggaagacgcttctaacgactatcagcgcgaagcgaagaaatgacgctcgaagctgac	594		
Dh 360	caaggaagacgcttctaacgactatcagcgcgaagcgaagaaatgacgctcgaagctgac	419		
Query 595	tttgcgctcgaagatgatactgaagcttatctggaagattctaacgctcgtgaatga	654		
Dh 420	tcttgctcgaagatgatactgaagcttatctggaagattctaacgctcgtgaatga	479		
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LOCUS	S71333		
DEFINITION	alpha 1,3 galactosyltransferase [New World monkeys, marmoset lymphoid cell line B95.8, mRNA Partial, 1141 nt].		
ACCESSION	S71333		
VERSION	S71333.1		GI:558051
KEYWORDS			
SOURCE	New World monkeys.		
ORGANISM	Platyrrhini Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates. 1 (bases 1 to 1131) Horton, R., Maccheroni A., Amatrak, F. and Galili, H., defining the minimal size of catalytically active primate alpha 1,3- galactosyltransferase: structure-function studies on the recombinant truncated enzyme glycobiology 4 (2), 194-201 (1994) 9431837		
JOURNAL MEDLINE	Genbank staff at the National Library of Medicine created this entry [NHLdb] githsq 1502701 from the original journal article. This sequence comes from Fig. 1, location comes from Fig. 1, 1..1131 /organism="Platyrrhini" /db_xref="taxon:9479" /cell_line="lymphoid cell line B95.8" 1..1131 /note="This sequence comes from Fig. 1: conceptual translation differs from the translation presented in the manuscript (251[iv>=51]; alpha 1,367" /codon_start=1 /product="alpha 1,3 galactosyltransferase" /protein_id="AA81587.2" /gb_xref "GI:7717225" /translaton="MNKVGKVLISMLVSTIVFWEYINSPEGSFLMVHSKNPVEDSSQKKMKWPEGMENNNIHNUGDEPLEDKERKEGDDTELRLMMKPKPRPEVATLVQWKAPVWBEGLYNKATLENTYAKOITVGLTVRIGRYIEHYLPREVI SARAYEVHGKPIFYVNWADVSKAPFIELGLRSFKVEFKPERKWDJSMRKRTIGEHLIAHIGHEVDPLFCMDWDVGFODHPGVETLQSVAQLQAMWYKADPDFTYERRKESAA YIPRGGDDEYTHAAIFGSTPIOVNLITOECKRIILDKKNIDIAEMHEDSHLNKYFLII NKPSKLISPEVCWYHHIGLSPLDIKTVMKSMTKRYNLYRRKV"		
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ACCESSION A69348
VERSION A69348.1 GI:4760175
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1065)
AUTHORS Goulet, P., Robberecht, P., Vandermee, A. and Woelbroeck, M.
TITLE PEPTIDE LIGANDS HAVING A HIGHER SELECTIVITY FOR THE VIP1 RECEPTOR
JOURNAL: Patent: WO 9802453-A 5, 22-JAN-1998;
UNIV BRUXELLES (BE)
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